

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Pastan, Ira
Chang, Kai
- (ii) TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Not yet assigned
(B) FILING DATE: Not yet assigned
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/776,271
(B) FILING DATE: 01-DEC-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/00224
(B) FILING DATE: 03-JAN-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/010,166
(B) FILING DATE: 05-JAN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Faris, Susan K.
(B) REGISTRATION NUMBER: 41,739
(C) REFERENCE/DOCKET NUMBER: 015280-259110US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 100..1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGGAATTCCG GTGGCCGGCC ACTCCCGTCT GCTGTGACGC GCGGACAGAG AGCTACCGGT	60
GGACCCACGG TGCCTCCCTC CCTGGGATCT ACACAGACC ATG GCC TTG CAA CGG	114
Met Ala Leu Gln Arg	
1 5	
CTC GAC CCC TGT TGG TCC TGT GGG GAC CGC CCT GGC AGC CTC CTG TTC	162
Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro Gly Ser Leu Leu Phe	
10 15 20	
CTG CTC TTC AGC CTC GGA TGG GTG CAT CCC GCG AGG ACC CTG GCT GGA	210
Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala Arg Thr Leu Ala Gly	
25 30 35	
GAG ACA GGG ACG GAG TCT GCC CCC CTG GGG GGA GTC CTG ACA ACC CCC	258
Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly Val Leu Thr Thr Pro	
40 45 50	
CAT AAC ATT TCC AGC CTC TCC CCT CGC CAA CTC CTT GGC TTC CCG TGT	306
His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu Leu Gly Phe Pro Cys	
55 60 65	
GCG GAG GTG TCC GGC CTG AGC ACG GAG CGT GTC CGG GAG CTG GCT GTG	354
Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val Arg Glu Leu Ala Val	
70 75 80 85	
GCC TTG GCA CAG AAG AAT GTC AAG CTC TCA ACA GAG CAG CTG CGC TGT	402
Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr Glu Gln Leu Arg Cys	
90 95 100	
CTG GCT CAC CGG CTC TCT GAG CCC CCC GAG GAC CTG GAC GCC CTC CCA	450
Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp Leu Asp Ala Leu Pro	
105 110 115	
TTG GAC CTG CTG CTA TTC CTC AAC CCA GAT GCG TTC TCG GGG CCC CAG	498
Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala Phe Ser Gly Pro Gln	
120 125 130	
GCC TGC ACC CGT TTC TTC TCC CGC ATC ACG AAG GCC AAT GTG GAC CTG	546
Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys Ala Asn Val Asp Leu	
135 140 145	

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CTC CCG AGG GGG GCT CCC GAG CGA CAG CGG CTG CTG CCT GCG GCT CTG Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu Leu Pro Ala Ala Leu 150 155 160 165	594
GCC TGC TGG GGT GTG CGG GGG TCT CTG CTG AGC GAG GCT GAT GTG CGG Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser Glu Ala Asp Val Arg 170 175 180	642
GCT CTG GGA GGC CTG GCT TGC GAC CTG CCT GGG CGC TTT GTG GCC GAG Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly Arg Phe Val Ala Glu 185 190 195	690
TCG GCC GAA GTG CTG CTA CCC CGG CTG GTG AGC TGC CCG GGA CCC CTG Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser Cys Pro Gly Pro Leu 200 205 210	738
GAC CAG GAC CAG CAG GAG GCA GCC AGG GCG GCT CTG CAG GGC GGG GGA Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala Leu Gln Gly Gly Gly 215 220 225	786
CCC CCC TAC GGC CCC CCG TCG ACA TGG TCT GTC TCC ACG ATG GAC GCT Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val Ser Thr Met Asp Ala 230 235 240 245	834
CTG CGG GGC CTG CTG CCC GTG CTG GGC CAG CCC ATC ATC CGC AGC ATC Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro Ile Ile Arg Ser Ile 250 255 260	882
CCG CAG GGC ATC GTG GCC GCG TGG CGG CAA CGC TCC TCT CGG GAC CCA Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg Ser Ser Arg Asp Pro 265 270 275	930
TCC TGG CGG CAG CCT GAA CGG ACC ATC CTC CGG CCG CGG TTC CGG CGG Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg Pro Arg Phe Arg Arg 280 285 290	978
GAA GTG GAG AAG ACA GCC TGT CCT TCA GGC AAG AAG GCC CGC GAG ATA Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys Lys Ala Arg Glu Ile 295 300 305	1026
GAC GAG AGC CTC ATC TTC TAC AAG AAG TGG GAG CTG GAA GCC TGC GTG Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu Leu Glu Ala Cys Val 310 315 320 325	1074
GAT GCG GCC CTG CTG GCC ACC CAG ATG GAC CGC GTG AAC GCC ATC CCC Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg Val Asn Ala Ile Pro 330 335 340	1122
TTC ACC TAC GAG CAG CTG GAC GTC CTA AAG CAT AAA CTG GAT GAG CTC Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His Lys Leu Asp Glu Leu 345 350 355	1170
TAC CCA CAA GGT TAC CCC GAG TCT GTG ATC CAG CAC CTG GGC TAC CTC Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln His Leu Gly Tyr Leu 360 365 370	1218
TTC CTC AAG ATG AGC CCT GAG GAC ATT CGC AAG TGG AAT GTG ACG TCC Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys Trp Asn Val Thr Ser 375 380 385	1266

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CTG GAG ACC CTG AAG GCT TTG CTT GAA GTC GAC AAA GGG CAC GAA ATG 1314
 Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp Lys Gly His Glu Met
 390 395 400 405

AGT CCT CAG GCT CCT CGG CGG CCC CTC CCA CAG GTG GCC ACC CTG ATC 1362
 Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln Val Ala Thr Leu Ile
 410 415 420

GAC CGC TTT GTG AAG GGA AGG GGC CAG CTA GAC AAA GAC ACC CTA GAC 1410
 Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp
 425 430 435

ACC CTG ACC GCC TTC TAC CCT GGG TAC CTG TGC TCC CTC AGC CCC GAG 1458
 Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu
 440 445 450

GAG CTG AGC TCC GTG CCC CCC AGC AGC ATC TGG GCG GTC AGG CCC CAG 1506
 Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln
 455 460 465

GAC CTG GAC ACG TGT GAC CCA AGG CAG CTG GAC GTC CTC TAT CCC AAG 1554
 Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys
 470 475 480 485

GCC CGC CTT GCT TTC CAG AAC ATG AAC GGG TCC GAA TAC TTC GTG AAG 1602
 Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys
 490 495 500

ATC CAG TCC TTC CTG GGT GGG GCC CCC ACG GAG GAT TTG AAG GCG CTC 1650
 Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu
 505 510 515

AGT CAG CAG AAT GTG AGC ATG GAC TTG GCC ACG TTC ATG AAG CTG CGG 1698
 Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg
 520 525 530

ACG GAT GCG GTG CTG CCG TTG ACT GTG GCT GAG GTG CAG AAA CTT CTG 1746
 Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu
 535 540 545

GGA CCC CAC GTG GAG GGC CTG AAG GCG GAG GAG CGG CAC CGC CCG GTG 1794
 Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val
 550 555 560 565

CGG GAC TGG ATC CTA CGG CAG CGG CAG GAC GAC CTG GAC ACG CTG GGG 1842
 Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly
 570 575 580

CTG GGG CTA CAG GGC GGC ATC CCC AAC GGC TAC CTG GTC CTA GAC CTC 1890
 Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu
 585 590 595

AGC GTG CAA GAG ACC CTC TCG GGG ACG CCC TGC CTC CTA GGA CCT GGA 1938
 Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly
 600 605 610

CCT GTT CTC ACC GTC CTG GCA CTG CTC CTA GCC TCC ACC CTG GCC 1983
 Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala
 615 620 625

TGAGGGCCCC ACTCCCTTGC TGGCCCCAGC CCTGCTGGGG ATCCCCGCCT GGCCAGGAGC 2043

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AGGCACGGGT GATCCCCGTT CCACCCCAAG AGAACTCGCG CTCAGTAAAC GGGAACATGC 2103
 CCCCTGCAGA CAAAAAAAAA AAAAAAAAAA AAAAA 2138

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Gln Arg Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro
 1 5 10 15
 Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala
 20 25 30
 Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly
 35 40 45
 Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu
 50 55 60
 Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val
 65 70 75 80
 Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr
 85 90 95
 Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp
 100 105 110
 Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala
 115 120 125
 Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys
 130 135 140
 Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu
 145 150 155 160
 Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser
 165 170 175
 Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly
 180 185 190
 Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser
 195 200 205
 Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala
 210 215 220
 Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val
 225 230 235 240

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Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro
 245 250 255
 Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg
 260 265 270
 Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg
 275 280 285
 Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys
 290 295 300
 Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu
 305 310 315 320
 Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg
 325 330 335
 Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His
 340 345 350
 Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln
 355 360 365
 His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys
 370 375 380
 Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp
 385 390 395 400
 Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln
 405 410 415
 Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp
 420 425 430
 Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys
 435 440 445
 Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp
 450 455 460
 Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp
 465 470 475 480
 Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser
 485 490 495
 Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu
 500 505 510
 Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr
 515 520 525
 Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu
 530 535 540
 Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu
 545 550 555 560

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Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp
 565 570 575

Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr
 580 585 590

Leu Val Leu Asp Leu Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys
 595 600 605

Leu Leu Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala
 610 615 620

Ser Thr Leu Ala
 625

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Gly Gly Gly Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Glu Asp Leu Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Glu Asp Leu
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Pro Arg Phe Arg Arg
1 5

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